

## Notic to Comply

Application No.

09/529,239

Examiner

David H Kruse

Applicant(s)

DOUTRIAUX ET AL.

Art Unit

1638

### NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

#### Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

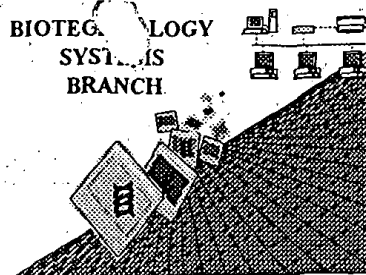
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#10/K.1  
7/5  
Raw  
Seq  
Listing  
(error)  
**RECEIVED**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/529,239

Source: 1638

Date Processed by STIC: 6-12-01

JUL 05 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

JUL 05 2001

TECH CENTER 1600/2900

1638

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

Does Not Comply  
Corrected Diskette Needed

See pp. 1, 2, 5

2 <110> APPLICANT: Doutriaux, Marie-Pascale  
3 Betzner, Andreas  
4 Freyssinet, Georges  
5 Perez, Pascal  
7 <120> TITLE OF INVENTION: METHOD FOR OBTAINING PLANT VARIETIES  
10 <130> FILE REFERENCE: A33153-PCT-USA 072667.0128  
12 <140> CURRENT APPLICATION NUMBER: US 09/529,239  
C--> 13 <141> CURRENT FILING DATE: 2000-01-27  
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06977  
16 <151> PRIOR FILING DATE: 1998-10-09  
18 <160> NUMBER OF SEQ ID NOS: 98

## ERRORED SEQUENCES

932 <210> SEQ ID NO: 26  
933 <211> LENGTH: 1385  
934 <212> TYPE: DNA  
935 <213> ORGANISM: Arabidopsis thaliana ecotype Columbia  
936 <223> OTHER INFORMATION: Clone 43  
938 <400> SEQUENCE: 26

→ Number of sequences differ.  
- 1385 listed  
- 2188 shown (see next page)

940 cccgggatgc agcgccagag atcgattttg tctttcttcc aaaaaccacac ggcggcgact	60
941 acgaagggtt tggtttcggy cgatgctgct agcgggcggy gcggcagcgy aggaccacga	120
942 tttaattgtga aggaagggya tgctaaaggc gacgcttctg tacgttttgc tgtttcgaaa	180
943 tctgtcgatg aggttagagg aacggatact ccaccggaga aggttcgcgy tctgtgctctg	240
944 cgtcttgatg ttaagccggy tgaatccgcy ggtgatgctt cgtccctggt ctccaatatt	300
945 atgcataagt ttgtaaaagt cgatgatcga gattgttctg gagagaggag ccgagaagat	360
946 gttgttcgcy tgaatgattc atctctatgt atgaaggcta atgatgttat tcttcaattt	420
947 cgttccaata atggtaaaac tcaagaaaga aaccatgctt ttagtttcag tgggagagct	480
948 gaacttagat cagtagaaga tataggagta gatggcgatg ttcctgggtc agaaacacca	540
949 gggatgcgcy cactgcttc tgccttgaag cgagttcttg aggatgaaat gacttttaag	600
950 gaggataagg ttctgtatt ggactctaac aaaaggctga aaatgctcca ggatccggtt	660
951 tgtggagaga agaaagaagt aaacgaagga accaaaattg aatggcttga gtcttctcga	720
952 atcagggatg ccaatagaag acgtcctgat gatccccctt acgatagaaa gaccttacac	780
953 ataccacctg atgttttcaa gaaaatgtct gcatacaaaa agcaatattg gagtgttaag	840
954 agtgaatata tggacattgt gcttttcttt aaagtgggga aattttatga gctgtatgag	900
955 ctagatgcgy aattaggtca caaggagctt gactggaaga tgaccatgag tgggtgaggga	960
956 aaatgcagac aggttggtat ctctgaaagt gggatagatg aggcagtgca aaagctatta	1020
957 gctcgtggat ataaagttgg acgaatcgag cagctagaaa catctgacca agcaaaagcc	1080
958 agaggtgcta atactataa tccaaggaag ctagttcagg tattaactcc atcaacagca	1140
959 agcgagggaa acatcgggcy tgatgccgcy catcttcttg ctataaaaaga gatcaaaatg	1200
960 gagctacaaa agtggttcaac tgtgtatgga tttgcttttg ttgactgtgc tgccttgagg	1260
961 ttttggttg ggtccatcag cgatgatgca tcatgtgctg ctcttgagc gttattgatg	1320
962 caggtttctc caaaggaagt gttatatgac agtaaaggcy tatcaagaga agcacaagag	1380
963 gctctaagg aatatacgtt gacagggtct acggcggtac agttggctcc agtaccacaa	1440
964 gtaatgggg atacagatgc tgctggagtt agaaatataa tagaatctaa cggatacttt	1500
965 aaaggttctt ctgaatcatg gaactgtgct gttgatggct taaatgaatg tgatgttgcc	1560

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

966 cttagtgtc ttggagagct aattaatcat ctgtctaggc taaagctaga agatgtactt 1620
967 aagcatgggg atatttttcc ataccaagtt tacaggggtt gtctcagaat tgatggccag 1680
968 acgatggtaa atcttgagat atttaacaat agctgtgatg gtggtccttc agggaccttg 1740
969 tacaaatatac ttgataactg tgttagtcca actggttaag gactcttaag gaattggatc 1800
970 tgccatccac tcaaagatgt agaaagcatc aataaacggc ttgatgtagt tgaagaattc 1860
971 acggcaaaact cagaaagtat gcaaatcact ggccagtatc tccacaaact tccagactta 1920
972 gaaagactgc tcggacgcat caagtctagc gttcgatcat cagcctctgt gttgcctgct 1980
973 cttctgggga aaaaagtgtc gaaacaacga gttaaagcat ttgggcaaat tgtgaaaggg 2040
974 ttcagaagtg gaattgatct gttgttggct ctacagaagg aatcaaatat gatgagtttg 2100
975 ctttataaac tctgtaaact tcctatatta gtaggaaaaa gcgggctaga gttatttctt 2160

```

E--&gt; 976 tctcaattcg aagcagceat agatagcg

2188

1013 &lt;210&gt; SEQ ID NO: 28

1014 &lt;211&gt; LENGTH: 34

1015 &lt;212&gt; TYPE: DNA

1016 &lt;213&gt; ORGANISM: Artificial sequence

1018 &lt;220&gt; FEATURE:

1019 &lt;223&gt; OTHER INFORMATION: MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis thaliana

1020 ecotype Columbia

E--&gt; 1022 &lt;400&gt; SEQUENCE: 26

1024 atccccgggtt atttgggaac acagtaagag gatt 34

1341 &lt;210&gt; SEQ ID NO: 31

1342 &lt;211&gt; LENGTH: 1109

1343 &lt;212&gt; TYPE: PRT

1344 &lt;213&gt; ORGANISM: Arabidopsis thaliana ecotype Columbia

1345 &lt;223&gt; OTHER INFORMATION: Polypeptide MSH6

1347 &lt;400&gt; SEQUENCE: 31

1349 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala

1350 1 5 10 15

1352 Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly

1353 20 25 30

1355 Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly

1356 35 40 45

1358 Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg

1359 50 55 60

1361 Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser

1362 65 70 75 80

1364 Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser

1365 85 90 95

1367 Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly

1368 100 105 110

1370 Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys

1371 115 120 125

1373 Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys

1374 130 135 140

1376 Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu

1377 145 150 155 160

1379 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu

1380 165 170 175

1382 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu

1385 listed.

Incorrect sequence i.d. number.

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Input Set : A:\09529239SeqList.txt

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1383		180		185		190
1385	Asp Glu Met Thr Phe Lys Glu Asp	Lys Val Pro Val Leu Asp Ser Asn				
1386	195	200	205			
1388	Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu					
1389	210	215	220			
1391	Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg					
1392	225	230	235	240		
1394	Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr					
1395	245	250	255			
1397	Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys					
1398	260	265	270			
1400	Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe					
1401	275	280	285			
1403	Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly					
1404	290	295	300			
1406	His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys					
1407	305	310	315	320		
1409	Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys					
1410	325	330	335			
1412	Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr					
1413	340	345	350			
1415	Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys					
1416	355	360	365			
1418	Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly					
1419	370	375	380			
1421	Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu					
1422	385	390	395	400		
1424	Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala					
1425	405	410	415			
1427	Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala					
1428	420	425	430			
1430	Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp					
1431	435	440	445			
1433	Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr					
1434	450	455	460			
1436	Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met					
1437	465	470	475	480		
1439	Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly					
1440	485	490	495			
1442	Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu					
1443	500	505	510			
1445	Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His					
1446	515	520	525			
1448	Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe					
1449	530	535	540			
1451	Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met					
1452	545	550	555	560		
1454	Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly					
1455	565	570	575			

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Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

```

1457 Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg
1458                      580                      585                      590
1460 Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile
1461                      595                      600                      605
1463 Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser
1464                      610                      615                      620
1466 Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg
1467 625                      630                      635                      640
1469 Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu
1470                      645                      650                      655
1472 Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe
1473                      660                      665                      670
1475 Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala
1476                      675                      680                      685
1478 Leu Gln Lys Glu Ser Asn Met Ser Leu Leu Tyr Lys Leu Cys Lys
1479                      690                      695                      700
1481 Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln
1482 705                      710                      715                      720
1484 Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
1485                      725                      730                      735
1487 Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
1488                      740                      745                      750
1490 Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
1491                      755                      760                      765
1493 Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
1494                      770                      775                      780
1496 Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
1497 785                      790                      795                      800
1499 Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His
1500                      805                      810                      815
1502 Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
1503                      820                      825                      830
1505 Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser
1506                      835                      840                      845
1508 Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
1509                      850                      855                      860
1511 Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
1512 865                      870                      875                      880
1514 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
1515                      885                      890                      895
1517 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
1518                      900                      905                      910
1520 Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
1521                      915                      920                      925
1523 Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
1524                      930                      935                      940
1526 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
1527 945                      950                      955                      960
1529 Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:50

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

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1530          965          970          975
1532 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
1533          980          985          990
1535 Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
1536          995          1000          1005
1538 Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val
1539          1010          1015          1020
1541 Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly
E--> 1542 1025          1030          1035          1040
1544 Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser
EOK> 1545          1045          1050          1055
1547 Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser
EOK> 1548          1060          1065          1070
1550 Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu
EOK> 1551          1075          1080          1085
1553 Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser
EOK> 1554          1090          1095          1100
EOK> 1556 Tyr Cys Val Pro Lys
EOK> 1557 1105

```

→ Amino acid  
number cannot  
be under two  
amino acids.

Move one space  
to the right.

→ Remaining lines are shown as  
erred due to the one error  
at amino 1040.

↓  
Gly  
1040

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001

TIME: 13:19:51

Input Set : A:\09529239SeqList.txt

Output Set: N:\CRF3\06122001\I529239.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1385 Found:2188 SEQ:26

L:1022 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:26

L:1542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31

M:332 Repeated in SeqNo=31